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UniProtKB/Swiss-Prot entry Q69ZS6

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Entry history

[Entry info] [Name and origin] [References] [Comments] [Cross-references]
[Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	SV2C_MOUSE
Primary accession number	Q69ZS6
Secondary accession numbers	None
Integrated into Swiss-Prot on	June 13, 2006
Sequence was last modified on	June 13, 2006 (Sequence version 2)
Annotations were last modified on	June 10, 2008 (Entry version 32)

Name and origin of the protein

Protein name	Synaptic vesicle glycoprotein 2C
Synonym	Synaptic vesicle protein 2C
Gene name	Name: Sv2c
	Synonyms: Kiaa1054
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gl Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mu
Protein existence	1: Evidence at protein level;

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Fetal brain;
DOI=10.1093/dnares/11.3.205; PubMed=15368895 [NCBI, ExPASy, EBI, Israel, Japan]
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Seino S.,
Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene: IV. The comple·
nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of
terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
DNA Res. 11:205-218(2004).

[2] INDUCTION.
DOI=10.1038/35087000; PubMed=11483953 [NCBI, ExPASy, EBI, Israel, Japan]
Xu T., Bajjalieh S.M.;
"SV2 modulates the size of the readily releasable pool of secretory vesicles.";
Nat. Cell Biol. 3:691-698(2001).

[3] TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
DOI=10.1002/cne.10636; PubMed=12687700 [NCBI, ExPASy, EBI, Israel, Japan]
Wang M.M., Janz R., Belizaire R., Frishman L.J., Sherry D.M.;
"Differential distribution and developmental expression of synaptic vesicle protein 2 isofor·
the mouse retina.";
J. Comp. Neurol. 460:106-122(2003).

[4] FUNCTION AS A BOTA RECEPTOR.
DOI=10.1016/j.febslet.2006.02.074; PubMed=16545378 [NCBI, ExPASy, EBI, Israel, Jap·
Mahrhold S., Rummel A., Bigalke H., Davletov B., Binz T.;
"The synaptic vesicle protein 2C mediates the uptake of botulinum neurotoxin A into phren
nerves.";
FEBS Lett. 580:2011-2014(2006).

[5] FUNCTION AS A BOTA RECEPTOR.
DOI=10.1126/science.1123654; PubMed=16543415 [NCBI, ExPASy, EBI, Israel, Japan]
Dong M., Yeh F., Tepp W.H., Dean C., Johnson E.A., Janz R., Chapman E.R.;
"SV2 is the protein receptor for botulinum neurotoxin A.";
Science 312:592-596(2006).

Comments

- *FUNCTION*: Plays a role in the control of regulated secretion in neural and endocrine c·
  enhancing selectively low-frequency neurotransmission. Positively regulates vesicle fus
  maintaining the readily releasable pool of secretory vesicles *(By similarity)*.
- *FUNCTION*: Receptor for the botulinium neurotoxin type A/BOTA.
- *SUBUNIT*: Interacts with SYT1 in a calcium-dependent manner *(By similarity)*.
- *SUBCELLULAR LOCATION*: Cytoplasmic vesicle, secretory vesicle, synaptic vesicle
  membrane; Multi-pass membrane protein *(By similarity)*. Note=Enriched in small synap·
  vesicles and adrenal microsomes, not present in chromaffin granules. Associated with ·
  insulin granules and synaptic-like microvesicles in insulin-secreting cells of the pancre·
  similarity).
- *TISSUE SPECIFICITY*: Expressed in specific subsets of conventional synapses in the r·
  (at protein level).
- *DEVELOPMENTAL STAGE*: Expressed during synaptogenesis in the retina (at protein
  level).
- *INDUCTION*: Up-regulated upon Sv2a depletion.
- *PTM*: N-glycosylated *(By similarity)*.
- *SIMILARITY*: Belongs to the major facilitator superfamily.

Copyright

Cross-references

Sequence databases

EMBL	AK173092; BAD32370.1; ALT_INIT; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
RefSeq	XP_996351.1; -.	
UniGene	Mm.441155	

3D structure databases

ModBase	Q69ZS6.

Organism-specific databases

MGI	MGI:1922459; Sv2c.
GeneLynx	Sv2c; Mus musculus.

Gene expression databases

ArrayExpress	Q69ZS6; -.
CleanEx	MM_SV2C; -.
GermOnline	ENSMUSG00000051111; Mus musculus.

Ontologies

GO	GO:0008021; Cellular component: synaptic vesicle *(inferred from direct assay MGI)*. GO:0007268; Biological process: synaptic transmission *(traceable author state from MGI)*. QuickGo view.

Family and domain databases

InterPro	IPR007114; MFS. IPR011701; MFS_1. IPR005988; SV2. Graphical view of domain structure.
PANTHER	PTHR11600:SF32; SV2; 1.
Pfam	PF07690; MFS_1; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01299; synapt_SV2; 1.
PROSITE	PS50850; MFS; 1. PROSITE graphical view of domain structure (profiles).
BLOCKS	Q69ZS6.

Genome annotation databases

Ensembl	ENSMUSG00000051111; Mus musculus. [Contig view]
GeneID	75209; -.
NMPDR	fig|10090.3.peg.28276; -.

Phylogenomic databases

HOVERGEN	Q69ZS6; -.

Other

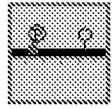|	
SOURCE	Sv2c; Mus musculus.
ROUGE	KIAA1054.

ProtoNet   Q69ZS6.
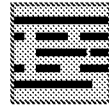UniRef   View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Cell junction; Cytoplasmic vesicle; Glycoprotein; Membrane; Neurotransmitter transpc
Receptor; Synapse; Transmembrane; Transport.

Features

Feature table viewer   Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	727	727	Synaptic vesicle glycoprotein 2C.	PRO_000023977
TOPO_DOM	1	154	154	Cytoplasmic (Potential).	
TRANSMEM	155	175	21	Potential.	
TOPO_DOM	176	191	16	Extracellular (Potential).	
TRANSMEM	192	212	21	Potential.	
TOPO_DOM	213	226	14	Cytoplasmic (Potential).	
TRANSMEM	227	247	21	Potential.	
TOPO_DOM	248	248	1	Extracellular (Potential).	
TRANSMEM	249	269	21	Potential.	
TOPO_DOM	270	280	11	Cytoplasmic (Potential).	
TRANSMEM	281	301	21	Potential.	
TOPO_DOM	302	320	19	Extracellular (Potential).	
TRANSMEM	321	341	21	Potential.	
TOPO_DOM	342	437	96	Cytoplasmic (Potential).	
TRANSMEM	438	458	21	Potential.	
TOPO_DOM	459	578	120	Extracellular (Potential).	
TRANSMEM	579	599	21	Potential.	
TOPO_DOM	600	609	10	Cytoplasmic (Potential).	
TRANSMEM	610	630	21	Potential.	
TOPO_DOM	631	636	6	Extracellular (Potential).	
TRANSMEM	637	657	21	Potential.	
TOPO_DOM	658	670	13	Cytoplasmic (Potential).	
TRANSMEM	671	693	23	Potential.	
TOPO_DOM	694	697	4	Extracellular (Potential).	
TRANSMEM	698	716	19	Potential.	
TOPO_DOM	717	727	11	Cytoplasmic (Potential).	
REGION	1	57	57	Interaction with SYT1 (By similarity).	
REGION	529	566	38	BOTA-binding (By similarity).	
CARBOHYD	480	480		N-linked (GlcNAc...) (Potential).	
CARBOHYD	484	484		N-linked (GlcNAc...) (Potential).	
CARBOHYD	534	534		N-linked (GlcNAc...) (Potential).	
CARBOHYD	559	559		N-linked (GlcNAc...) (Potential).	
CARBOHYD	565	565		N-linked (GlcNAc...) (Potential).	

Sequence information

Length: 727 AA [This is the   Molecular weight: 82291 Da

length of the unprocessed precursor]

[This is the MW of the unprocessed precursor]

CRC64: E1D78203D4E3183A is a checksum on the sequenc

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        10         20         30         40         50         60
MEDSYKDRTS LMKGAKDIAK EVKKQTVKKV NQAVDRAQDE YTQRSYSRFQ DEEDDDDYYP

        70         80         90        100        110        120
PGETYSGEVN DDEGSSEATE GHDEEDEIYE GEYQGIPSTN QGKDSIVSVG QPKGDEYKDR

       130        140        150        160        170        180
RELESERRAD EEELAQQYEL IIQECGHGRF QWALFFVLGM ALMADGVEVF VVGFVLPSAE

       190        200        210        220        230        240
TDLCIPNSGS GWLGSIVYLG MMVGAFFWGG LADKVGRKQS LLICMSVNGF FAFLSSFVQG

       250        260        270        280        290        300
YGFFLVCRLL SGFGIGGAIP TVFSYFAEVL AREKRGEHLS WLCMFWMIGG IYASAMAWAI

       310        320        330        340        350        360
IPHYGWSFSM GSAYQFHSWR VFVIVCALPC VSSVVALTFM PESPRFLLEV GKHDEAWMIL

       370        380        390        400        410        420
KLIHDTNMRA RGQPEKVFTV NKIKTPKQID ELIEIESDTG TWYRRCFVRI RTELYGIWLT

       430        440        450        460        470        480
FMRCFNYPVR ENTIKLTIVW FTLSFGYYGL SVWFPDVIKH LQSDEYALLT RNVQKDKYAN

       490        500        510        520        530        540
FSINFTMENQ IHTGMEYENG RFLGVKFKSV TFKDSVFKSC TFDDVTSVNT YFKNCTFIDT

       550        560        570        580        590        600
LFDNTDFEPY KFIDSEFQNC SFLHNKTGCQ ITFDDDYSAY WIYFVNFLGT LAVLPGNIVS

       610        620        630        640        650        660
ALLMDRIGRL TMLGGSMVLS GISCFFLWFG TSESMMIGML CLYNGLTISA WNSLDVVTVE

       670        680        690        700        710        720
LYPTDRRATG FGFLNALCKA AAVLGNLIFG SLVSITKAIP ILLASTVLVC GGLVGLRLPD

TRTQVLM
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BLAST   ExPASy/SIB
or at NCBI (USA)

ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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analysis tools

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